STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/541,626*
Source: *IFWO*
Date Processed by STIC: *4/27/06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
       http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
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Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/541,626_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 _____ Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
Numbering   use **space characters**, instead.

4 _____ Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
ensure your subsequent submission is saved in ASCII text.**

5 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.**

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES)   <210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
is Artificial Sequence. (see item 11 below)

11 _____ Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
Sequence Rules

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/541,626

DATE: 04/27/2006
TIME: 09:14:14

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04272006\J541626.raw

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 3 <110> APPLICANT: Haruo HANAWA
 5 <120> TITLE OF INVENTION: VECTOR FOR GENE THERAPY AND METHOD OF QUANTIFYING
TARGET PROTEIN IN
 6        MAMMAL OR CULTURED CELLS WITH THE ADMINISTRATION OF THE VECTOR FOR
GENE
 7        THERAPY
 9 <130> FILE REFERENCE: 0760-0347PUS1
11 <140> CURRENT APPLICATION NUMBER: US 10/541,626
12 <141> CURRENT FILING DATE: 2005-07-07
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/016956
15 <151> PRIOR FILING DATE: 2003-12-26
17 <150> PRIOR APPLICATION NUMBER: JP 2003-3967
18 <151> PRIOR FILING DATE: 2003-01-10
20 <160> NUMBER OF SEQ ID NOS: 24
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 11
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: oligopeptide encoding C19-29 region of glucagon of
human, mouse or rat
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33 1               5                   10
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37 <211> LENGTH: 1471
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: DNA insert encoding rat IFN-r receptor, rat IgG Fc
region and glucagon
43        C19-29 region
46 <220> FEATURE:
47 <221> NAME/KEY: CDS
48 <222> LOCATION: (13)..(1461)
49 <223> OTHER INFORMATION: DNA insert encoding rat IFN-r receptor, rat IgG Fc
region and glucagon
50        C19-29 region
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55                1               5                   10
57 ggg agt gga gct ttg atg agc acc gag gat cct aag ccg ccc tcg gtg      99
58 Gly Ser Gly Ala Leu Met Ser Thr Glu Asp Pro Lys Pro Pro Ser Val
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59      15                    20                    25
61 cct gcg cca aca aat gtt cta att acg tcc tat gac ttg aac cct gtc        147
62 Pro Ala Pro Thr Asn Val Leu Ile Thr Ser Tyr Asp Leu Asn Pro Val
63 30                    35                    40                    45
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RAW SEQUENCE LISTING   DATE: 04/27/2006
PATENT APPLICATION: US/10/541,626   TIME: 09:14:14

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04272006\J541626.raw

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69 cag gta aag atg tat cca gaa tac tgg act gat gcc tgc acc aac att    243
70 Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile
71             65                  70                  75
73 gcc cat cat tat tgt aat atc tac aaa cac att tcc tat cct gac tca    291
74 Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser
75             80                  85                  90
77 tct gcc tgg gcc aga gtt aag gcc aag gtt gga caa aga gaa tct gcc    339
78 Ser Ala Trp Ala Arg Val Lys Ala Lys Val Gly Gln Arg Glu Ser Ala
79     95                  100                 105
81 tat gcg cag tca gaa gag ttt att atg tgc cga aag ggg aag gtt gga    387
82 Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly
83 110                 115                 120                 125
85 ccg cct ggc ctg gac atc gga agg aag gaa gat cag ctg att gtc cac    435
86 Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His
87             130                 135                 140
89 ata ttt cac cct aag gtc aat gtg agt cag gaa acc atg ttt ggt gac    483
90 Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp
91             145                 150                 155
93 gga aat acc tgt tac aca ttc gac tac act gtg ttt gtg aaa cat tac    531
94 Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr
95             160                 165                 170
97 agg agt ggg gag atc cta cat aca gaa cat agc gtc cta aaa gaa gat    579
98 Arg Ser Gly Glu Ile Leu His Thr Glu His Ser Val Leu Lys Glu Asp
99     175                 180                 185
101 tgt agc gaa act ctg tgt gag tta aac atc tca gtg tcc acg ctg aat    627
102 Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn
103 190                 195                 200                 205
105 tcc aat tac tgt gtt tca gta gtt gga aag tcg tct ttc tgg caa gtt    675
106 Ser Asn Tyr Cys Val Ser Val Val Gly Lys Ser Ser Phe Trp Gln Val
107             210                 215                 220
109 aat aca gaa aca tca aaa gac gcc tgt atc ccc ttt ctc cat gat gac    723
110 Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp
111             225                 230                 235
113 aga gaa gaa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc aag    771
114 Arg Glu Glu Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys
115             240                 245                 250
117 cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc ccc    819
118 Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe Pro
119     255                 260                 265
121 cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg    867
122 Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr
123 270                 275                 280                 285
125 tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc agc    915
126 Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe Ser
127             290                 295                 300
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130 Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro Pro
131         305                 310                 315
133 gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc atc   1011
134 Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
135         320                 325                 330
137 ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc acc   1059
138 Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val Thr
139         335                 340                 345
141 agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc gaa   1107
142 Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Glu
143 350                 355                 360                 365
145 ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag gaa   1155
146 Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys Glu
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151             385                 390                 395
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154 Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro Gln
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158 Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser Tyr
159         415                 420                 425
161 ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag gga   1347
162 Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln Gly
163 430                 435                 440                 445
165 aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat   1395
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167             450                 455                 460
169 act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt gtg   1443
170 Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe Val
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183 <220> FEATURE:
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191 ccaacgaccc cgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag   180
193 ggactttcca ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac   240
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197 cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg   360
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/27/2006
PATENT APPLICATION: US/10/541,626   TIME: 09:14:15

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04272006\J541626.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes
spaces.

Seq#:9; Line(s) 846
Seq#:10; Line(s) 858
Seq#:11; Line(s) 870
Seq#:12; Line(s) 882
Seq#:23; Line(s) 1023
Seq#:24; Line(s) 1035

VERIFICATION SUMMARY   DATE: 04/27/2006
PATENT APPLICATION: US/10/541,626   TIME: 09:14:15

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04272006\J541626.raw